

What is claimed is:

1. A method for analyzing gene expression comprising:
obtaining expression levels of a plurality of genes;
selecting at least one biological characteristic from a plurality of biological
characteristics stored in a database; wherein the biological characteristics comprise
5 genomic information about the genes, structural information about the products of the
genes; and biological function of the genes; and
analyzing the expression levels according to the selected at least one biological
characteristic.
- 10 2. The method of Claim 1 wherein the analyzing comprises grouping the expression
levels according to the selected at least one biological characteristic.
3. The method of Claim 1 wherein the analyzing comprises selecting the expression
levels for further analysis according to the selected at least one biological
15 characteristic.
4. The method of Claim 1 wherein the analyzing comprises clustering according to
selected at least one biological characteristic.
- 20 5. The method of Claim 4 wherein the analyzing comprises multiple dimensional
clustering according to selected biological characteristics.

6. The method of Claim 6 wherein the analyzing comprises data mining.

7. The method of Claim 1 wherein the plurality of biological characteristics comprise orthologous genes.

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8. The method of Claim 1 wherein the plurality of biological characteristics comprise pathologic characteristics of genes.

9. The method of Claim 1 wherein the plurality of biological characteristics comprise splice variant information.

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10. The method of Claim 1 wherein the plurality of biological characteristics comprise protein domain information.

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11. The method of Claim 1 wherein the plurality of biological characteristics comprise signal pathway information.

12. The method of Claim 1 wherein the plurality of biological characteristics comprise gene ontology information.

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13. The method of Claim 1 wherein the database is a relational database.

14. The method of Claim 1 wherein the database is an object oriented database.

15. The method of Claim 13 wherein the biological characteristics are retrieved using SQL statements.

16. A system for analyzing gene expression comprising a processor; and a memory
5 being coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform the method steps of obtaining expression levels of a plurality of genes;

selecting at least one biological characteristic from a plurality of biological characteristics stored in a database; wherein the biological characteristics comprise
10 genomic information about the genes, structural information about the products of the genes; and biological function of the genes; and analyzing the expression levels according to the selected at least one biological characteristic.

17. The system of Claim 16 wherein the analyzing comprises grouping the expression levels according to the selected at least one biological characteristic.

18. The system of Claim 16 wherein the analyzing comprises selecting the expression levels for further analysis according to the selected at least one biological
20 characteristic.

19. The system of Claim 16 wherein the analyzing comprises clustering according to selected at least one biological characteristic.

20. The system of Claim 16 wherein the analyzing comprises multiple dimensional clustering according to selected biological characteristics.

5 21. The system of Claim 16 wherein the analyzing comprises data mining.

22. The system of Claim 16 wherein the plurality of biological characteristics comprise orthologous genes.

10 23. The system of Claim 16 wherein the plurality of biological characteristics comprise pathologic characteristics of genes.

24. The system of Claim 16 wherein the plurality of biological characteristics comprise splice variant information.

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25. The system of Claim 16 wherein the plurality of biological characteristics comprise protein domain information.

20 26. The system of Claim 16 wherein the plurality of biological characteristics comprise signal pathway information.

27. The system of Claim 16 wherein the plurality of biological characteristics comprise gene ontology information.

28. The system of Claim 16 wherein the database is a relational database.

29. The system of Claim 16 wherein the database is an object oriented database.

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30. The system of Claim 28 wherein the biological characteristics are retrieved using SQL statements.

31. A computer readable medium comprising computer-executable instructions for performing the methods comprising:

obtaining expression levels of a plurality of genes;

selecting at least one biological characteristic from a plurality of biological characteristics stored in a database; wherein the biological characteristics comprise genomic information about the genes, structural information about the products of the genes; and biological function of the genes; and

analyzing the expression levels according to the selected at least one biological characteristic.

32. The computer readable medium of Claim 31 wherein the analyzing comprises grouping the expression levels according to the selected at least one biological characteristic.

33. The computer readable medium of Claim 31 wherein the analyzing comprises selecting the expression levels for further analysis according to the selected at least one biological characteristic.

5 34. The computer readable medium of Claim 31 wherein the analyzing comprises clustering according to selected at least one biological characteristic.

35. The computer readable medium of Claim 31 wherein the analyzing comprises multiple dimensional clustering according to selected biological characteristics.

10 36. The computer readable medium of Claim 31 wherein the analyzing comprises data mining.

15 37. The computer readable medium of Claim 31 wherein the plurality of biological characteristics comprise orthologous genes.

38. The computer readable medium of Claim 31 wherein the plurality of biological characteristics comprise pathologic characteristics of genes.

20 39. The computer readable medium of Claim 31 wherein the plurality of biological characteristics comprise splice variant information.

40. The computer readable medium of Claim 31 wherein the plurality of biological characteristics comprise protein domain information.
41. The computer readable medium of Claim 31 wherein the plurality of biological characteristics comprise signal pathway information.
42. The computer readable medium of Claim 31 wherein the plurality of biological characteristics comprise gene ontology information.
43. The computer readable medium of Claim 31 wherein the database is a relational database.
44. The computer readable medium of Claim 31 wherein the database is an object oriented database.
45. The computer readable medium of Claim 43 wherein the biological characteristics are retrieved using SQL statements.